R. Shukla

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RAW SEQUENCE LISTING   DATE: 07/21/2000
PATENT APPLICATION: US/09/321,987A   TIME: 07:58:44

Input Set : A:\Sequence
Output Set: N:\CRF3\07212000\I321987A.raw

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 3 <110> APPLICANT: Kimble, Judith E
 4        Blelloch, Robert H
 6 <120> TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
 8 <130> FILE REFERENCE: 960296.95386
10 <140> CURRENT APPLICATION NUMBER: 09/321987A
11 <141> CURRENT FILING DATE: 1999-05-28
13 <150> PRIOR APPLICATION NUMBER: 60/087170
14 <151> PRIOR FILING DATE: 1998-05-29
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 6659
22 <212> TYPE: DNA
23 <213> ORGANISM: Caenorhabditis elegans
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(6450)
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31 Met Arg Ser Ile Gly Gly Ser Phe His Leu Leu Gln Pro Val Val Ala
32   1               5                  10                  15
34 gct ctc ata ctc ctc gtc gtc tgc ctc gtt tat gcg ttg caa tca ggg    96
35 Ala Leu Ile Leu Leu Val Val Cys Leu Val Tyr Ala Leu Gln Ser Gly
36              20                  25                  30
38 agt ggc acg atc tca gaa ttc tca tca gat gtg ctg ttc tcc agg gcc   144
39 Ser Gly Thr Ile Ser Glu Phe Ser Ser Asp Val Leu Phe Ser Arg Ala
40          35                  40                  45
42 aag tac tca ggt gtg cca gtg cat cac agt cga tgg cgt caa gac gcc   192
43 Lys Tyr Ser Gly Val Pro Val His His Ser Arg Trp Arg Gln Asp Ala
44      50                  55                  60
46 ggt ata cac gtc atc gac agc cat cac atc gtc cga aga gat tct tat   240
47 Gly Ile His Val Ile Asp Ser His His Ile Val Arg Arg Asp Ser Tyr
48   65                  70                  75                  80
50 gga cgt cgt gga aaa cgt gat gtc acg tca aca gat cgg cga cgt cga   288
51 Gly Arg Arg Gly Lys Arg Asp Val Thr Ser Thr Asp Arg Arg Arg Arg
52                  85                  90                  95
54 ctc caa gga gtt gcc aga gac tgt gga cat gct tgt cac tta cga tta   336
55 Leu Gln Gly Val Ala Arg Asp Cys Gly His Ala Cys His Leu Arg Leu
56              100                 105                 110
58 cga tca gat gat gcc gtc tac atc gtt cat ttg cac aga tgg aat caa   384
59 Arg Ser Asp Asp Ala Val Tyr Ile Val His Leu His Arg Trp Asn Gln
60          115                 120                 125
62 ata ccg gac tca cat aac aaa agt gtt ccc cac ttt tcc aat tca aat   432
63 Ile Pro Asp Ser His Asn Lys Ser Val Pro His Phe Ser Asn Ser Asn
64      130                 135                 140
66 ttc gcg ccg atg gtc tta tat ttg gac tcg gag gag gag gtt aga ggt   480
67 Phe Ala Pro Met Val Leu Tyr Leu Asp Ser Glu Glu Glu Val Arg Gly
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68 145                    150                    155                    160
70 gga atg tct cga aca gat ccc gat tgt atc tac cgt gca cac gtt aaa    528
71 Gly Met Ser Arg Thr Asp Pro Asp Cys Ile Tyr Arg Ala His Val Lys
72                    165                    170                    175
74 ggt gta cat cag cac agc atc gtc aat tta tgc gac tcg gaa gac gga    576
75 Gly Val His Gln His Ser Ile Val Asn Leu Cys Asp Ser Glu Asp Gly
76                    180                    185                    190
78 ttg tac gga atg ctt gca cta ccc agc gga atc cat acg gtt gag cca    624
79 Leu Tyr Gly Met Leu Ala Leu Pro Ser Gly Ile His Thr Val Glu Pro
80           195                    200                    205
82 att att agt gga aac gga aca gag cac gac gga gca agt cgc cat agg    672
83 Ile Ile Ser Gly Asn Gly Thr Glu His Asp Gly Ala Ser Arg His Arg
84       210                    215                    220
86 caa cat ctc gtc cga aag ttc gat cca atg cac ttc aaa tcg ttt gac    720
87 Gln His Leu Val Arg Lys Phe Asp Pro Met His Phe Lys Ser Phe Asp
88 225                    230                    235                    240
90 cat ctt aac tcg acc agt gtc aac gag acg gag acg acg gtt gcc acg    768
91 His Leu Asn Ser Thr Ser Val Asn Glu Thr Glu Thr Thr Val Ala Thr
92                    245                    250                    255
94 tgg caa gat cag tgg gaa gat gtt att gaa cgc aaa gca aga tcc cga    816
95 Trp Gln Asp Gln Trp Glu Asp Val Ile Glu Arg Lys Ala Arg Ser Arg
96                    260                    265                    270
98 aga gct gcc aac tct tgg gat cac tat gtt gaa gtc ctt gtg gtg gcg    864
99 Arg Ala Ala Asn Ser Trp Asp His Tyr Val Glu Val Leu Val Val Ala
100           275                    280                    285
102 gat aca aaa atg tac gaa tat cac gga aga tct ctt gaa gac tac gtt   912
103 Asp Thr Lys Met Tyr Glu Tyr His Gly Arg Ser Leu Glu Asp Tyr Val
104       290                    295                    300
106 ctc act ctc ttc tcc aca gtt gcc tcc atc tat cgt cac caa tcc ctt   960
107 Leu Thr Leu Phe Ser Thr Val Ala Ser Ile Tyr Arg His Gln Ser Leu
108 305                    310                    315                    320
110 cgt gca tct atc aat gtc gtt gtt gtc aag ttg atc gtt ttg aaa acg   1008
111 Arg Ala Ser Ile Asn Val Val Val Val Lys Leu Ile Val Leu Lys Thr
112                    325                    330                    335
114 gaa aac gct gga cca cga atc act cag aac gct caa caa aca ctt caa   1056
115 Glu Asn Ala Gly Pro Arg Ile Thr Gln Asn Ala Gln Gln Thr Leu Gln
116                    340                    345                    350
118 gat ttc tgt aga tgg cag cag tat tac aat gat cca gat gat tcg agt   1104
119 Asp Phe Cys Arg Trp Gln Gln Tyr Tyr Asn Asp Pro Asp Asp Ser Ser
120           355                    360                    365
122 gtc caa cat cat gac gtt gca atc ctt ttg acg cgt aaa gat att tgt   1152
123 Val Gln His His Asp Val Ala Ile Leu Leu Thr Arg Lys Asp Ile Cys
124       370                    375                    380
126 cga tca caa gga aaa tgc gat aca ctt gga ctt gct gaa ctt gga aca   1200
127 Arg Ser Gln Gly Lys Cys Asp Thr Leu Gly Leu Ala Glu Leu Gly Thr
128 385                    390                    395                    400
130 atg tgt gat atg caa aaa agt tgt gca atc ata gaa gac aat gga ttg   1248
131 Met Cys Asp Met Gln Lys Ser Cys Ala Ile Ile Glu Asp Asn Gly Leu
132                    405                    410                    415
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134 agt gct gca ttc aca att gct cat gaa ttg ggt cat gtg ttt tcg att   1296
135 Ser Ala Ala Phe Thr Ile Ala His Glu Leu Gly His Val Phe Ser Ile
136         420             425             430
138 cct cat gat gac gaa cga aaa tgc tct acc tac atg ccg gtt aat aag   1344
139 Pro His Asp Asp Glu Arg Lys Cys Ser Thr Tyr Met Pro Val Asn Lys
140         435             440             445
142 aac aac ttc cac ata atg gca cca acg ttg gaa tat aac act cat cca   1392
143 Asn Asn Phe His Ile Met Ala Pro Thr Leu Glu Tyr Asn Thr His Pro
144         450             455             460
146 tgg agt tgg tcg cca tgt tca gct gga atg ctc gaa cga ttc ctc gaa   1440
147 Trp Ser Trp Ser Pro Cys Ser Ala Gly Met Leu Glu Arg Phe Leu Glu
148 465             470             475             480
150 aat aat cga ggt caa act caa tgt cta ttc gat cag ccg gtc gaa cgt   1488
151 Asn Asn Arg Gly Gln Thr Gln Cys Leu Phe Asp Gln Pro Val Glu Arg
152             485             490             495
154 cgt tac tac gag gat gtc ttt gta cgt gat gaa cca gga aag aaa tac   1536
155 Arg Tyr Tyr Glu Asp Val Phe Val Arg Asp Glu Pro Gly Lys Lys Tyr
156         500             505             510
158 gat gct cat caa cag tgc aag ttt gta ttt gga cca gct tct gag ttg   1584
159 Asp Ala His Gln Gln Cys Lys Phe Val Phe Gly Pro Ala Ser Glu Leu
160         515             520             525
162 tgc cct tat atg ccg aca tgc cgc cgt ctt tgg tgt gca aca ttc tac   1632
163 Cys Pro Tyr Met Pro Thr Cys Arg Arg Leu Trp Cys Ala Thr Phe Tyr
164         530             535             540
166 gga agc cag atg ggc tgt cga act cag cat atg cca tgg gcc gac gga   1680
167 Gly Ser Gln Met Gly Cys Arg Thr Gln His Met Pro Trp Ala Asp Gly
168 545             550             555             560
170 act cct tgt gac gaa tca aga agc atg ttc tgt cat cat gga gcc tgt   1728
171 Thr Pro Cys Asp Glu Ser Arg Ser Met Phe Cys His His Gly Ala Cys
172             565             570             575
174 gtt cgt cta gcc ccc gaa tcc ctt acc aaa att gac gga caa tgg ggt   1776
175 Val Arg Leu Ala Pro Glu Ser Leu Thr Lys Ile Asp Gly Gln Trp Gly
176         580             585             590
178 gac tgg cga tca tgg gga gaa tgc agt cgt act tgt ggt ggt ggt gtt   1824
179 Asp Trp Arg Ser Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly Gly Val
180         595             600             605
182 caa aaa gga tta aga gat tgt gac agc cca aaa cct cga aat ggt gga   1872
183 Gln Lys Gly Leu Arg Asp Cys Asp Ser Pro Lys Pro Arg Asn Gly Gly
184         610             615             620
186 aag tac tgt gtt ggt caa cga gaa cgt tat cgg tca tgt aat aca caa   1920
187 Lys Tyr Cys Val Gly Gln Arg Glu Arg Tyr Arg Ser Cys Asn Thr Gln
188 625             630             635             640
190 gaa tgc cca tgg gat act caa cca tac cgt gaa gtt caa tgt tct gaa   1968
191 Glu Cys Pro Trp Asp Thr Gln Pro Tyr Arg Glu Val Gln Cys Ser Glu
192             645             650             655
194 ttc aac aat aaa gat att gga atc caa ggt gtc gct tca acg aat act   2016
195 Phe Asn Asn Lys Asp Ile Gly Ile Gln Gly Val Ala Ser Thr Asn Thr
196         660             665             670
198 cac tgg gtt cca aaa tat gcg aat gtt gca cca aat gaa cgt tgc aag   2064
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199 His Trp Val Pro Lys Tyr Ala Asn Val Ala Pro Asn Glu Arg Cys Lys
200         675             680             685
202 ctg tat tgt cgg ctc agt gga tct gca gcg ttc tat ctg ctt cga gat    2112
203 Leu Tyr Cys Arg Leu Ser Gly Ser Ala Ala Phe Tyr Leu Leu Arg Asp
204     690             695             700
206 aaa gtt gtt gat gga aca cca tgt gat aga aat gga gac gat att tgt    2160
207 Lys Val Val Asp Gly Thr Pro Cys Asp Arg Asn Gly Asp Asp Ile Cys
208 705             710             715             720
210 gta gct gga gct tgt atg cca gca ggc tgt gat cat caa ctt cat tca    2208
211 Val Ala Gly Ala Cys Met Pro Ala Gly Cys Asp His Gln Leu His Ser
212             725             730             735
214 act ctc cga aga gac aaa tgt ggt gtt tgc ggt ggg gat gat tct tcc    2256
215 Thr Leu Arg Arg Asp Lys Cys Gly Val Cys Gly Gly Asp Asp Ser Ser
216             740             745             750
218 tgt aag gtt gtc aaa gga aca ttt aat gag caa gga acc ttt ggt tat    2304
219 Cys Lys Val Val Lys Gly Thr Phe Asn Glu Gln Gly Thr Phe Gly Tyr
220         755             760             765
222 aac gaa gta atg aag att cca gct ggt tct gca aat att gat atc cgg    2352
223 Asn Glu Val Met Lys Ile Pro Ala Gly Ser Ala Asn Ile Asp Ile Arg
224     770             775             780
226 cag aaa gga tat aat aat atg aaa gaa gat gac aat tat ctt tct ctc    2400
227 Gln Lys Gly Tyr Asn Asn Met Lys Glu Asp Asp Asn Tyr Leu Ser Leu
228 785             790             795             800
230 cgt gcc gcc aat ggt gaa ttc cta ctt aac ggt cat ttc caa gta tca    2448
231 Arg Ala Ala Asn Gly Glu Phe Leu Leu Asn Gly His Phe Gln Val Ser
232             805             810             815
234 ctg gct cgc caa caa att gca ttc caa gac act gtt ctc gaa tat tct    2496
235 Leu Ala Arg Gln Gln Ile Ala Phe Gln Asp Thr Val Leu Glu Tyr Ser
236             820             825             830
238 ggt tct gat gca att att gaa cgg ata aat gga act ggt ccg att aga    2544
239 Gly Ser Asp Ala Ile Ile Glu Arg Ile Asn Gly Thr Gly Pro Ile Arg
240         835             840             845
242 agt gac att tat gtt cat gtt ctt tct gtt ggt agt cat cca ccc gac    2592
243 Ser Asp Ile Tyr Val His Val Leu Ser Val Gly Ser His Pro Pro Asp
244     850             855             860
246 atc tca tat gag tac atg act gcg gct gtt cca aat gct gta att cgg    2640
247 Ile Ser Tyr Glu Tyr Met Thr Ala Ala Val Pro Asn Ala Val Ile Arg
248 865             870             875             880
250 cca ata tcc agt gca ttg tat ttg tgg aga gtt acg gat act tgg aca    2688
251 Pro Ile Ser Ser Ala Leu Tyr Leu Trp Arg Val Thr Asp Thr Trp Thr
252             885             890             895
254 gaa tgt gat aga gcc tgt cgt gga cag caa tcg caa aaa tta atg tgt    2736
255 Glu Cys Asp Arg Ala Cys Arg Gly Gln Gln Ser Gln Lys Leu Met Cys
256         900             905             910
258 ctg gac atg tcg act cat cgt caa agt cat gat aga aat tgt caa aat    2784
259 Leu Asp Met Ser Thr His Arg Gln Ser His Asp Arg Asn Cys Gln Asn
260     915             920             925
262 gtt ctc aaa cca aaa caa gca aca cga atg tgc aat ata gat tgt tct    2832
263 Val Leu Lys Pro Lys Gln Ala Thr Arg Met Cys Asn Ile Asp Cys Ser
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264      930                    935              940
266 aca aga tgg atc act gaa gat gtg tct agt tgt agt gcc aaa tgt gga   2880
267 Thr Arg Trp Ile Thr Glu Asp Val Ser Ser Cys Ser Ala Lys Cys Gly
268 945                    950              955              960
270 tct gga cag aaa cgt caa cga gtt tct tgc gta aaa atg gag ggt gat   2928
271 Ser Gly Gln Lys Arg Gln Arg Val Ser Cys Val Lys Met Glu Gly Asp
272                    965              970              975
274 cgt caa act cca gca tcc gaa cat cta tgt gat cgt aat tca aaa cca   2976
275 Arg Gln Thr Pro Ala Ser Glu His Leu Cys Asp Arg Asn Ser Lys Pro
276                980              985              990
278 tcc gat att gcc agt tgt tac att gac tgc tct gga aga aaa tgg aac   3024
279 Ser Asp Ile Ala Ser Cys Tyr Ile Asp Cys Ser Gly Arg Lys Trp Asn
280            995              1000             1005
282 tat gga gaa tgg act tca tgt tct gaa act tgc gga tcg aat gga aaa   3072
283 Tyr Gly Glu Trp Thr Ser Cys Ser Glu Thr Cys Gly Ser Asn Gly Lys
284     1010             1015             1020
286 atg cat cgg aag tca tat tgc gtt gat gat tcg aat cgt cga gtt gat   3120
287 Met His Arg Lys Ser Tyr Cys Val Asp Asp Ser Asn Arg Arg Val Asp
288 1025             1030             1035             1040
290 gag tca ttg tgc ggc aga gaa cag aaa gag gcg aca gaa cgg gaa tgt   3168
291 Glu Ser Leu Cys Gly Arg Glu Gln Lys Glu Ala Thr Glu Arg Glu Cys
292             1045             1050             1055
294 aac aga att cca tgt cca aga tgg gtt tat ggg cat tgg tca gag tgc   3216
295 Asn Arg Ile Pro Cys Pro Arg Trp Val Tyr Gly His Trp Ser Glu Cys
296             1060             1065             1070
298 tct cga agt tgt gat ggt gga gtc aaa atg cgt cat gct caa tgt ttg   3264
299 Ser Arg Ser Cys Asp Gly Gly Val Lys Met Arg His Ala Gln Cys Leu
300     1075             1080             1085
302 gat gca gcc gat cgg gaa aca cat aca tcc aga tgt ggt cca gca cag   3312
303 Asp Ala Ala Asp Arg Glu Thr His Thr Ser Arg Cys Gly Pro Ala Gln
304     1090             1095             1100
306 aca caa gaa cat tgt aat gaa cat gct tgt act tgg tgg cag ttc gga   3360
307 Thr Gln Glu His Cys Asn Glu His Ala Cys Thr Trp Trp Gln Phe Gly
308 1105             1110             1115             1120
310 gtc tgg tct gac tgc tca gct aag tgt gga gat ggt gta cag tat cga   3408
311 Val Trp Ser Asp Cys Ser Ala Lys Cys Gly Asp Gly Val Gln Tyr Arg
312             1125             1130             1135
314 gac gct aat tgt acc gat cgt cat aga tca gta cta ccg gaa cat cgt   3456
315 Asp Ala Asn Cys Thr Asp Arg His Arg Ser Val Leu Pro Glu His Arg
316     1140             1145             1150
318 tgc ctt aaa atg gaa aag ata att aca aaa cca tgt cat aga gaa tca   3504
319 Cys Leu Lys Met Glu Lys Ile Ile Thr Lys Pro Cys His Arg Glu Ser
320     1155             1160             1165
322 tgt cca aaa tat aaa ctt gga gaa tgg tct cag tgt agt gtt tct tgt   3552
323 Cys Pro Lys Tyr Lys Leu Gly Glu Trp Ser Gln Cys Ser Val Ser Cys
324 1170             1175             1180
326 gag gat gga tgg tcg tca aga aga gtt tca tgt gtt tct gga aat gga   3600
327 Glu Asp Gly Trp Ser Ser Arg Arg Val Ser Cys Val Ser Gly Asn Gly
328 1185             1190             1195             1200
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VERIFICATION SUMMARY   DATE: 07/21/2000
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